CHAPTER 1

PUBLIC HEALTH IMPACT OF FOODBORNE ILLNESS: IMPETUS FOR THE INTERNATIONAL FOOD SAFETY EFFORT

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1.1 INTRODUCTION

Microbial food safety has emerged as a global concern because of its effect on consumer health and the financial losses in the food industry due to product recalls and trade barriers. In the United States the economic impact of foodborne illness, although secondary to the loss of lives, is driven by medical care, legal fees, public health investigation, lost wages, loss of market share, and loss of consumer confidence and is estimated at $20 to $43 billion each year (USDHHS, continuously updated). In this chapter we survey the impact of foodborne pathogens—viral, bacterial, fungal, and protozoan—at the global dinner table and provide a brief overview of foodborne morbidity and mortality with examples based primarily on data for the United States. This will set the table for more in-depth descriptions in the following chapters of the epidemiology, food safety issues in specific commodities, methods for detection, prevention and control strategies, risk assessments, and global impact of each pathogen on the food supply.

1.2 STATISTICAL ESTIMATES

The World Health Organization (WHO) estimates that in 2005, 1.8 million people died from diarrheal disease, with a significant proportion of these cases following the consumption of contaminated food and drinking water (WHO, continuously updated-a). In the United States up to 30% of the population experiences foodborne illnesses,

TABLE 1   Estimated Public Health Impact of Foodborne Illnesses in the United States and the Proportion for Which an Etiology Is Known

	Cases	Hospitalizations	Deaths
Etiology unknown	62 million	265,000	3,200
Etiology known	14 million	60,000	1,800
Total	76 million	325,000	5,000

Source: Mead et al. (1999).

as evidenced by the 76 million cases, 325,000 hospitalizations, and 5000 deaths estimated annually (Table 1).

Nearly 81.6%—62 million cases, 265,000 hospitalizations, and 3200 deaths—have no known cause (Table 1). For the approximately 18% of foodborne illnesses for which an etiology is known (Table 2) viruses such as norovirus, rotavirus, and hepatitis virus cause the overwhelming majority (79.3%) of human morbidity followed by bacteria (13.5%) and protozoans (6.6%) (Mead et al., 1999).

Foodborne illnesses occur as single sporadic cases or as outbreaks involving two or more persons who consumed the same product in the same time interval. Based on data from the Centers for Disease Control and Prevention (CDC), the vehicles of transmission causing 67% of U.S. outbreaks remain unknown. Of the remaining 33% of outbreaks for which an etiology was identified, fruits, vegetables, and salads, including ready-to-eat packaged products (22%), shellfish (22%), and poultry (5%) rank as the top three vehicles of transmission (CDC, continuously updated).

Recently published attribution data and per capita consumption provide insight into the relative importance of specific commodities as vehicles of foodborne pathogens (Table 3). As illustrated in the following chapters, multiple pathogens contaminate a variety of food types. Thus, *Listeria monocytogenes*, which has been described in major epidemics involving dairy products, is associated with cases incriminating contaminated ready-to-eat delicatessen items, seafood, and produce.

TABLE 2   Estimated Morbidity and Mortality of Foodborne Illnesses in the United States

	Cases	Deaths
Norwalk-like viruses	9,200,000	124
Campylobacter	1,963,141	91
Salmonella	1,342,532	556
Toxoplama gondii	112,500	375
Yersinia	86,731	2
E. coli O1578:H7	62,458	52
E. coli STEC	31,229	26
Listeria monocytogenes	2,493	449

Source: Mead et al. (1999).

TABLE 3   Mean Number of Cases of Foodborne Illness Attributed to Specific Foods and Estimated per Capita Consumption

	Total Cases	Percent	Per Capita Consumption[a] (lb)
Produce	3,800,929	29.4	688.6
Seafood	3,200,976	24.8	16.1
Poultry	2,036,156	15.8	73.5
Luncheon meats	921,538	7.1	NA
Breads, bakery items	543,714	4.2	192.3
Dairy	535,566	4.1	38.0
Eggs	446,964	3.5	253.9
Beverages (nondairy)	444,020	3.4	142 gal
Beef	437,051	3.4	62.4
Pork	402,217	3.1	46.4
Game	140,473	1.1	NA

Source: Hoffman et al. (2007), USDA-ERS (2007a).
[a]NA, per capita consumption not available from USDA Economic Research Service.

TABLE 4   U.S. Public Health Service Targeted Reductions in Major Foodborne Pathogens (Cases per 100,000 U.S. Population)

	1987	2000	2010
Campylobacter jejuni	50	25	12.3
Salmonella spp.	18	16	6.8
E. coli O157:H7	8	4	1.0
Listeria monocytogenes	0.7	0.5	0.25

Source: USDHHS (continuously updated).

To improve the overall health of the nation, the U.S. Department of Health and Human Services has set national goals for reducing human illness attributed to each of the major bacterial foodborne pathogens (Table 4). Targeted reductions use the 1987 baseline data for comparison and to project the goals to be achieved in Healthy People 2010 and in Healthy People 2020.

1.3   IMPACT OF REPRESENTATIVE FOODBORNE PATHOGENS

1.3.1   *Campylobacter jejuni*

Campylobacter jejuni is the leading cause of human bacterial foodborne illness worldwide. In 2004, the 25 member states of the European Union (EU) reported 183,961 cases of campylobacteriosis. The overall incidence of 47.6 cases/100,000 population represented a 31% increase from 2003. A trend toward increasing incidence was

observed in the 13 of the original 15 member states, with only Spain and Sweden reporting a decline. In the EU, 20 to 50% of all clinical isolates were resistant to fluoroquinolones, tetracyclines, and penicillin. Thus, the use of fluoroquinolones in food animals was banned to prevent the emergence of fluoroquinolone resistance (El Amin, 2006).

In the United States the nearly 2 million human campylobacteriosis cases account for an estimated $1.2 billion in productivity losses annually. Based on attribution data, contaminated poultry (72%), dairy products (7.8%), and red meats, including beef (4.3%) and pork (4.4%), are vehicles of transmission and acknowledged risk factors (Hoffman et al., 2007; Miller and Mandrell, 2005). In the Netherlands, Campylobacter Risk Management and Assessment (CARMA) is a multidisciplinary project to integrate information from risk assessments, epidemiology, and economics. CARMA estimates the cost of campylobacateriosis at 21 million euros annually, with an estimated 20 to 40% of cases attributed to contaminated poultry (Havelaar et al., 2007). The importance of pork in the transmission of *Campylobacter* (as well as of *Salmonella* and *Yersinia*) has been reviewed (Fosse et al., 2008). Other factors, such as water, contact with pets, and worldwide travel, loom as significant.

Campylobacteriosis has been linked with the onset of Guillain–Barré syndrome (GBS) (Buzby et al., 1997). Of an estimated 2628 to 9575 patients diagnosed with GBS in the United States, 526 to 3830 (20 to 40%) are triggered by *Campylobacter* infection in the 1 to 2 weeks prior to the onset of neurological symptoms (Rees et al., 1995). No single factor appears to cause a greater proportion of GBS cases than recent *Campylobacter* infections.

The availability of the total genome map (1.5×10^6 base pairs, ca. 1.5 megabases, Mb) of *C. jejuni* (Parkhill et al., 2000) and other food-associated *Campylobacter* species has expedited molecular-based methods for their detection, epidemiology, and pathogenesis. The impact of modern agricultural production practices on the convergence of *C. jejuni* and *C. coli* into a single species has been described (Sheppard et al., 2008). *Arcobacter butzleri*, a close relative of *Campylobacter*, is an emerging foodborne pathogens whose genetic makeup encodes traits to (2.34 Mb) ensure survival in a potentially hostile environment (Miller et al., 2007) such as a packing plant.

1.3.2 Nontyphoidal *Salmonella*

There are about 2500 serotypes of *Salmonella enterica*. Of these, a small fraction account for the majority of 1,343,000 cases of foodborne illness resulting in about 15,000 hospitalizations and 500 deaths annually in the United States (Mead et al., 1999). CDC has targeted reduction of human salmonellosis from 18 cases per 100,000 population in 1987 to 6.8 cases per 100,000 by the year 2010 (Table 4). In the EU, 192,703 cases of salmonellosis were reported during 2004. The 2004 incidence (42.4 cases/100,000 population) is an increase over 2003 prior to the admission of 10 new member states. Eggs, poultry, and pork are major sources of contamination; surveys show high *Salmonella* contamination in herbs and spices. The implementation of

control programs in the original member states has resulted in a decline in salmonellosis (El Amin, 2006).

In the United States, human salmonellosis follows consumption of contaminated poultry (35%), eggs (22%), and produce (12%), as well as beef (23.2%) and pork (5.7%), (Hoffman et al., 2007). The U.S. Department of Agriculture (USDA) Economic Research Service (ERS) estimates the annual losses in illness and productivity at $2.9 billion (USDA-ERS, 2007b).

Hazard analysis of critical control points (HACCP) was initiated in 1996 in USDA-inspected processing plants. In 1998, 10.65% of the overall number of regulatory samples analyzed by the USDA Food Safety and Inspection Service (FSIS) yielded *Salmonella*, compared with 4.29% in 2002 (Rose et al., 2002). The decline in human morbidity during this interval coincided with the reduction of *Salmonella* isolated from meat and poultry and may be attributed to the HACCP plans implemented by the industry (Eblen et al., 2005; USDA-FSIS, 1999). Because reduction of human salmonellosis is lagging behind that of other bacterial foodborne infections, in 2007 the USDA-FSIS further accelerated the targeted reduction of human salmonellosis by 50%.

The availability of the full *Salmonella* genome (4.8 Mb) will yield robust techniques for elucidating its pathogenesis and molecular epidemiology. Advances in rapid detection, serotyping, and virulence characterization will contribute significantly to comprehensive risk assessments and to evaluating the effectiveness of HACCP interventions both on-farm and during processing.

1.3.3 *E. coli* O157:H7

Human infections have been attributed to beef (67%) as well as to fruit juices, sprouts, lettuce, and spinach (18.4%) (Hoffman et al., 2007). Hemolytic uremic syndrome (HUS), a rare sequela of *E. coli* O157:H7 infection, is now listed as a separate entity targeted for reduction in the Healthy People 2010 document. For the year 2000, USDA-ERS calculated the costs of *E. coli* O157:H7 ($659 million) and non-O157:H7 ($329.7 million) (USDA-ERS, 2007b). The genome of enterohemorrhagic *E. coli* is estimated at 5 Mb. The significance of pathogenic *E. coli* is detailed in subsequent chapters.

1.3.4 *Listeria monocytogenes*

Listeria monocytogenes accounts for about 2500 cases, 2289 hospitalizations, and 449 deaths each year in the United States. The mortality rate of *L. monocytogenes* (ca. 28%) remains the highest of all foodborne pathogens (Table 2). The USDA-ERS estimates the cost of acute illness at $2.3 billion annually (USDA-ERS, 2007b). In the EU, 12,678 cases of listeriosis were reported in 2004, an incidence rate of 0.3 case/100,000 population. In countries with several years of data, the incidence of listeriosis increased compared with the preceding five years. In the EU, significant contamination (100 *L. monocytogenes*/gram) was reported in fishery products, meats,

cheeses, and ready-to-eat products, thus banning their import into the United States, which maintains a "zero tolerance" policy (El Amin, 2006).

Major human listeriosis epidemics have been linked to consumption of dairy products (Painter and Slutsker, 2007). Product recalls, sporadic cases, and outbreaks have incriminated ready-to-eat delicatessen items. Recent data attribute human listeriosis to consumption of contaminated delicatessen meats (54%), dairy products, including cheeses (24%), and produce (8.7%) (Hoffman et al., 2007). In France, listeriosis outbreaks have been traced to pickled pork tongue and involved 279 human cases (33% pregnancy-related) (Jacquet et al., 1995).

The full genome of *L. monocytogenes* (2.9 Mb) was published in 2001 by Glaser and colleagues (Glaser et al., 2001). This led to the development of microarray technologies to compare virulence attributes of strains and to single nucleotide polymorphism (SNP) analysis to track listeriosis dissemination. In addition, *prfA* virulence gene cluster sequence analysis assigned *L. monocytogenes* isolates to groups or lineages: clinical (lineage 1) and food-processing environments (lineage 3) (Ward et al., 2004). Earlier, molecular methods established that *Listeria* spp. persist in processing environments, including chilling and cutting rooms, knives, conveyer belts, and floor drains (Giovannacci et al., 1999). By pulsed field gel electrophoresis (PFGE), a multistate outbreak of human listeriosis, ascribed to serotype 4 (101 cases, resulting in 22 deaths), was linked to delicatessen meats prepared in a contaminated processing plant (CDC, 1998).

1.3.5 *Yersinia enterocolitica*

Pigs are the major animal reservoir for strains of *Y. enterocolitica* which are pathogenic to humans (Andersen et al. 1991; Bottone, 1997, 1999; Nielsen and Wegener, 1997). *Y. enterocolitica* is isolated from porcine tongue, tonsils, cecum, rectum, feces, and gut-associated lymphoid tissue, as well as from chitterlings and retail-purchased pork.

Attribution data link human yersiniosis to consumption of pork (71%), dairy products (12.2%), and seafoods (4.7%) (Hoffman et al., 2007). The public health risks associated with *Yersinia* on hog carcasses have been detailed (Fosse et al., 2008). Foodborne outbreaks have involved consumption or handling of contaminated raw or undercooked ground pork, pork tongues, and chitterlings (Bottone, 1999). During 1982, 172 cases of *Y. enterocolitica* serotype O:13a,13b were traced to pasteurized milk possibly contaminated with pig manure during transport (Robins-Browne, 2001). In addition to pork consumption, the risk of human yersiniosis in Auckland increased with contact with untreated water and sewage (Satterthwaite et al., 1999).

In the United States, human yersiniosis (96,368 cases, 1228 hospitalizations) is one of the seven major foodborne diseases under surveillance by CDC. According to FoodNet, the yersiniosis case rate (cases per 100,000 population) varies from 0.5 (California) to 3 (Georgia). The hospitalization rate for yersiniosis (32% of cases) is second only to that of listeriosis (94% of cases) (CDC, 2006). In 2004, the 25

TABLE 5 Percent Change of the Seven Bacterial Pathogens Under FoodNet Surveillance

	Cases/100,000	Percent Change	Confidence (%) Interval
Yersinia	0.36	−49	36–59
Shigella	4.67	−43	18–60
Listeria	0.30	−32	16–45
Campylobacter	12.72	−30	25–35
STEC 0157	1.06	−29	12–42
Salmonella	14.55	−9	2–15
Vibrio	0.27	+41	3–92

Source: CDC (2006).

member states of the EU reported 10,000 cases of human yersiniosis. The genome of *Y. enterocolitica* is estimated at 4.6 Mb by the Sanger Institute.

1.3.6 *Vibrio*

Vibrio cholerae is a major public health problem in developing countries. In addition to water, contaminated rice, vegetables, and seafoods have been implicated in cholera outbreaks (WHO, continuously updated-a). *Vibrio vulnificus* and *V. parahaemolyticus* are discussed in later chapters. In the United States, despite the overall reduction in foodborne pathogens since FoodNet was initiated in 1996, only seafood-related *Vibrio parahaemoliticus* cases have increased: by 41% (Table 5).

1.3.7 Parasites

FoodNet initiated national surveillance of parasitic infections in 1997. *Cyclospora cayetanensis* was first recognized as a foodborne pathogen in raspberries imported from Central America in 1996. Human cases are attributed to contaminated produce (96%), with fewer attributed to beverages (1.5%) (Hoffman et al., 2007). *Cryptosporodium parvum*, linked to municipal water supply outbreaks, has been also been traced to produce (59%) and beverages (9%) (Hoffman et al., 2007).

Toxoplasma gondii, which is transmitted between cats and domestic livestock and wildlife, has been associated with human infections traced to pork (41%), beef (23.2%), and produce (7%). Cats excrete the resistant oocysts in their feces. Infection occurs when pigs or other livestock ingest the oocysts, which invade skeletal muscle or other organs (i.e., brain, heart, liver). Humans become infected when eating contaminated meat or by inhaling or ingesting the oocyst released by the feline host. In the EU, 2000 cases of toxoplasmosis were reported in 2004; 225,000 cases were estimated in the United States (Mead et al., 1999). The genome of *T. gondii* is estimated at 30 Mb.

In 2004 the EU reported between 300 and 400 cases of *Trichinella*; 52 cases were estimated in the United States. In the EU, 300 to 400 cases due to *Echinococcus* were reported in 2004.

1.4   NATIONAL MICROBIAL BASELINE SURVEYS

In 1996–1998, the USDA Food Safety and Inspection Service conducted nationwide microbial baseline surveys of beef, hogs, poultry, and turkey carcasses and their respective ground meat products (see Chapter 8, Table 1). The data show the highest contamination of poultry carcasses with *Campylobacter* (90%), distribution of *Salmonella* across commodities, and *L. monocytogenes* in ground products, which may reflect contamination of the processing environment.

Baseline prevalence estimates will change for each pathogen as bacteriological methods for their isolation and molecular protocols for their detection improve and HACCP strategies in the plant evolve. Data obtained during these nationwide baseline studies are the basis for performance standards which serve as benchmarks for the industry as they optimize their HACCP strategies. Although the current emphasis is pathogen reduction at the processing level, reducing the on-farm prevalence of potential human pathogens will clearly result in an overall decline in human foodborne illness.

1.5   GLOBAL MARKETPLACE

In 2004, international trade in agricultural products (including food) was estimated at $783 billion, with the EU ($374 billion) being the largest importer. The United States imports 13% of its annual food or food ingredients, an estimated 260 lb of its yearly per capita diet, valued at $70 billion, principally from the EU, Canada, and Mexico. Approximately 1% of foods imported into the United States are inspected or tested by the U.S. Food and Drug Administration (FDA). Because of the emergence of China as an exporter of agricultural products, the FDA now has personnel assigned to Beijing.

International standards for food hygiene are coordinated through the multinational *Codex Alimentarius* (FAO/WHO, continuously updated). The *Codex* was founded in 1962 by the Food and Agriculture Committee of the United Nations and the World Health Organization. *Codex* committees set standards to protect the health of the global consumer and to ensure fair trade practices. *Codex* provides guidance to governments on methods to be used between laboratories to determine equivalencies, especially for export and import concerns.

To estimate the human burden of foodborne illnesses worldwide, the World Health Organization (WHO) coordinates efforts to compile laboratory, outbreak, and surveillance data from member nations (Flint et al., 2005; WHO, continuously updated-a). WHO Global Sal-Surv (WHO, continuously updated-b) collects prevalence data for *Salmonella*, *Campylobacter*, *Shigella*, bovine spongiform encephalopathy (BSE), and antimicrobial drug resistance profiles. In 2000, Australia launched OzFood Net to more accurately determine the burden of foodborne illness. This effort estimated that 5.4 million cases of foodborne gastroenteritis occur each year in Australia (AGDHA, 2005). Fourteen pathogens (11 bacterial and 3 viral) were monitored during 2000.

Major causes of gastroenteritis were pathogenic *E. coli* (38%), noroviruses (30%), and *Campylobacter* (14%).

FoodNet continuously monitors seven bacterial foodborne pathogens in 10 U.S. states, representing 44.5 million people or 15% of the population (Table 5) (Jones et al., 2007; Scallan et al., 2007). Six of the seven bacterial pathogens have shown reductions since FoodNet was initiated in 1997. Only seafood-related *Vibrio* cases have increased significantly (CDC, 2006).

Molecular-based approaches have accelerated detection and characterization of foodborne pathogens (Hytia-Trees et al., 2007; Withee and Dearfield, 2007). The availability of published full genome sequences available on the World Wide Web for *V. cholerae* (2.9 Mb), *Cryptosporidium* (9.1 Mb), and the protozoan *Giardia lamblia* (11.19 Mb), as well as of potential foodborne pathogens such as *Mycobacterium avium* subspecies paratuberculosis, will identify novel sequences for their rapid identification and hasten assessment of their human public health significance.

In the future, international multilaboratory and mulitnational collaborations utilizing state-of-the-art molecular protocols will yield reliable estimates of the morbidity and mortality associated with foodborne infections. Prevalence data for rigorous risk assessments will ensure the integrity of the global food supply.

When reviewing the following chapters the reader should be mindful that as-yet-unidentified foodborne pathogens may appear in future editions of this book. In addition, the global marketplace is confounded with production issues including limitations for the on-farm use of antimicrobials, transport of pathogens due to world travel, and animal welfare concerns. All of these affect the microbial food safety of the final product in the global market.

REFERENCES

AGDHA (Australian Government Department of Health and Ageing) (2005): Foodborne illness in Australia: annual incidence circa 2000. http://www.ozfoodnet.org.au/internet/ozfoodnet/publishing.nsf/Content/reports-1/$FILE/foodborne_report.pdf. Accessed June 2008.

Andersen JK, Sorensen R, Glensbjerg M (1991): Aspects of the epidemiology of *Yersinia enterocolitica*: a review. *Int J Food Microbiol*. 13:231–237.

Bottone EJ (1997): *Yersinia enterocolitica*: the charisma continues. *Clin Microbiol Rev*. 10:257–276.

——— (1999): *Yersinia enterocolitica*: overview and epidemiologic correlates. *Microb Infect*. 1:323–333.

Buzby JC, Roberts T, Allos BM (1997): *Estimated Annual Costs of* Campylobacter-*Associated Guillain–Barré Syndrome*. Publication 756. USDA-ERS, Washington, DC.

CDC (Centers for Disease Control and Prevention) (1998): Multistate outbreak of listeriosis—United States. *MMWR Morb Mortal Wkly Rep*. 47:1085–1086.

——— (2006): Preliminary FoodNet data on the incidence of infection with pathogens transmitted commonly through food: 10 states, United States, 2005. *MMWR Morb Mortal Wkly Rep*. 55:392–395.

————— (continuously updated): Outbreak surveillance data. http://www.cdc.gov/foodborneoutbreaks/outbreak_data.htm. Accessed May 2008.

Eblen DR, Levine P, Rose BE, Saini P, Mageau R, Hill WE (2005): Nationwide microbiological baseline data collected by sponge sampling during 1997 and 1998 for cattle, swine, turkeys, and geese. *J Food Prot*. 68:1848–1852.

El Amin A (2006): Foodborne *Campylobacter* infections increase. http://www.food-productiondaily.com/news/ng.asp?n=64828-food-safety-zoonoses-campylobacteria. Accessed June 2008.

FAO/WHO (Food and Agriculture Organization/World Health Organization) (continuously updated): *Codex Alimentarius*. http://www.codexalimentarius.net/web/index_en.jsp. Accessed June 2008.

Flint JA, vam Duynhoven YT, Angulo FJ, et al. (2005): Estimating the burden of acute gastroenteritis, foodborne disease, and pathogens commonly transmitted by food: an international review. *Clin Infect Dis*. 41:698–704.

Fosse J, Seegers H, Magras C (2008): Foodborne zoonoses due to meat: a quantitative approach for a comparative risk assessment applied to pig slaughtering in Europe. *Vet Res*. 39, E-pub ahead of print.

Giovannacci I, Ragimbeau C, Quequiner S, et al. (1999): *Listeria monocytogenes* in pork slaughtering and cutting plants: use of RAPD, PFGE and PCR-REA for tracing and molecular epidemiology. *Int J Food Microbiol*. 53:127–140.

Glaser P, Fangeul L, Buchrieser C, et al. (2001): Comparative genomics of *Listeria* species. *Science*. 294:849–852.

Havelaar AH, Mangen MJ, de Koeijer AA, et al. (2007): Effectiveness and efficiency of controlling *Campylobacter* on broiler chicken meat. *Risk Anal*. 27:831–844.

Hoffman S, Fischbeck P, Krupnick A, McWilliam M (2007): Using expert elicitation to link foodborne illnesses in the United States to foods. *J Food Prot*. 70:1220–1229.

Hytia-Trees EK, Cooper K, Ribot EM, Gerner-Smidt P (2007): Recent developments and future prospects in subtyping of foodborne bacterial pathogens. *Future Microbiol*. 2: 175–185.

Jacquet C, Catimel BR, Brosch R, et al. (1995): Investigations related to the epidemic strain involved in the French listeriosis outbreak in 1992. *Appl Environ Microbiol*. 61:2242–2246.

Jones TF, Scallan E, Angulo FJ (2007): FoodNet: overview of a decade of achievement. *Foodborne Pathol Dis*. 4:60–66.

Mead PS, Slutsker L, Dietz V, et al. (1999): Food-related illness and death in the United States. *Emerg Infect Dis*. 5:607–625.

Miller WG, Mandrell RE (2005): Prevalence of *Campylobacter* in the food and water supply: incidence, outbreaks, isolation, and detection. In: Ketley J, Konkel ME (Eds.). Campylobacter: *Molecular and Cellular Biology*. Horizon Bioscience, Norfolk, UK, pp. 101–163.

Miller WG, Parker CT, Rubenfield M, et al. (2007): The complete genome sequence and analysis of the epsilonproteobacterium *Arcobacater butzleri*. *PLoS One*. 26e1358.

Nielsen B, Wegener HC (1997): Public health and pork and pork products: regional perspectives of Denmark. *Rev Sci Tech Off Int Epizoot*. 16; 513–524.

Painter J, Slutsker L (2007): Listeriosis in humans. In: Marth E, Ryser E (Eds.). *Listeria, Listeriosis and Food Safety*, 3rd ed. CRC Press, Boca Raton, FL, pp. 85–109.

Parkhill J, Wren BW, Mungall K, et al. (2000): The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences. *Nature*. 402:665–668.

Rees JH, Soudain SE, Gregson NA, Hughes RAC (1995): *Campylobacter jejuni* infection and Guillain–Barré syndrome. *N Engl J Med.* 333:1374–1379.

Robins-Browne RM (2001): *Yersinia enterocolitica.* In: Doyle MP, Beuchat LR, Montville TJ (Eds.). *Food Microbiology: Fundamentals and Frontiers*, 2nd ed. ASM Press, Washington, DC, pp. 215–245.

Rose BE, Hill WE, Umholtz R, Ransom GM, James WO (2002): Testing for *Salmonella* in raw meat and poultry products collected at federally inspected establishments in the United States, 1998 through 2000. *J Food Prot.* 65:937–947.

Satterthwaite P, Pritchard K, Floyd D, Law B (1999): A case–control study of *Yersinia enterocolitica* infections in Auckland. *Aust NZ J Public Health.* 23:482–485.

Scallan E (2007): Activities, Achievements and lessons learned during the first 10 years of the Foodborne Dieases Active Surveillance Network: 1996–2005. *Clin Infect Dis.* 44:718–725.

Sheppard SK, McCarthy ND, Falush D, Maiden MVC (2008): Convergence of *Campylobacter* species; implications for bacterial evolution. *Science.* 320:237–239.

USDA-ERS (U.S. Department of Agriculture–Economic Research Service) (2007a): Food availability (per capita) data system. http://www.ers.usda.gov/data/foodconsumption. Accessed May 2008.

———— (2007b): Briefing rooms. http://www.ers.usda.gov/briefing/FoodSafety. Accessed May 2008.

USDA-FSIS (U.S. Department of Agriculture–Food Safety and Inspection Service) (1999): HACCP Implementation: first year *Salmonella* test results. http://www.fsis.usda.gov/OPHS/haccp/salmdata.htm. Accessed June 2008.

USDHHS (U.S. Department of Health and Human Services) (continuously updated): Healthy People 2010. http://www.healthypeople.gov/Data. Accessed February 2008.

Ward TJ, Gorski L, Borucki MK, Mandrell RE, Hutchins J, Pupedis K (2004): Intraspecific phylogeny and lineage group identification based on the *prfA* virulence gene cluster of *Listeria monocytogenes. J Bacteriol.* 186:4994–5002.

WHO (World Health Organization) (continuously updated-a): Media Centre. http://www.who.int/mediacentre/en. Accessed June 2008.

———— (continuously updated-b): Global Salm-Surv (GSS) site. http://www.who.int/salmsurv/en. Accessed June 2008.

Withee J, Dearfield KL (2007): Genomics-based food-borne pathogen testing and diagnostics: possibilities for the US Department of Agriculture's Food Safety and Inspection Service. *Environ Mol Mutagen.* 48:363–378.